

STIC-Biotech/ChemLib

141529

From: Sullivan, Daniel
Sent: Thursday, December 30, 2004 12:29 PM
To: STIC-Biotech/ChemLib
Subject: Request 09963803

Please search for the following in the pending, issued patent and commercial databases.

A nucleic acid comprising SEQ ID NO: 2

Thank you.

Daniel M. Sullivan

Examiner AU 1636
Remsen Bldg.
Room 2A74

Tel: (571) 272-0779

Mailbox: 2C70

CRFB

STAFF USE ONLY

Searcher: _____
Searcher Phone: 2- _____
Date Searcher Picked up: 1/3/05
Date Completed: _____
Searcher Prep/Rev. Time: _____
Online Time: _____

Type of Search

NA Sequence: # 1
AA Sequence: # _____
Structure: # _____
Bibliographic: _____
Litigation: _____
Patent Family: _____
Other: _____

Vendors and cost where applicable

STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: 09
WWW/Internet: _____
Other(Specify): _____

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OM nucleic - nucleic search, using sw model

Run on: January 5, 2005, 00:39:34 ; Search time 2589 Seconds
(without alignment)
7248.537 Million cell updates/sec

Title: US-09-963-803-2

Perfect score: 515

Sequence: 1 ccagaagaagtaattcccaag.....cagaagaattctgaatttcg 515

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

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2: gb_est2.*
3: gb_hic.*
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5: gb_est4.*
6: gb_est5.*
7: gb_est6.*
8: gb_gsa1.*
9: gb_gsa2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	62	12.0	540	8	AZ032908 RPCI-23-3
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4	59.8	11.6	629	9	CNS04EYV AL287681 Tetradon
5	59.6	11.6	625	9	CE633607 tigr-g88-CE633607 tigr-g88-
6	59.6	11.6	683	9	CE830234 tigr-g88-AL061936 Drosophila
7	59.2	11.5	1101	9	CNS00214 AL176953 Tetradon
8	58.8	11.4	907	9	CNS02147 AL176953 Tetradon
9	58.2	11.3	416	8	AZ652793 1M0526J10
10	58	11.3	336	8	AZ635799 1M0493108
11	58	11.3	432	9	CE704975 tigr-g88-AL564376 AL564376
12	58	11.1	981	1	AL564376 RPCI-24-1
13	57.2	11.1	473	8	AZ891439 RPCI-24-1
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15	57.2	11.1	775	9	AG602876 Mus muscu
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17	56.6	11.0	707	8	AZ985865 2M0267C20
18	56.4	11.0	571	9	CE097846 tigr-g88-AG310954 Mus muscu
19	56.4	11.0	1250	9	AZ408774 1M0180D24
20	56.2	10.9	440	8	CE197701 tigr-g88-CE197701 tigr-g88-
21	56.2	10.9	877	9	CR253706 Forward 8
22	56.2	10.9	877	9	CR253706 Forward 8
23	56	10.9	486	9	CE764895 tigr-g88-AL108367 Drosophila
24	56	10.9	639	9	CNS0170D

25	56	10.9	666	6	BY751847 BY751847
26	55.8	10.8	1008	9	CL059735 CH216-90U
27	55.8	10.8	1101	9	CNS004T2 AL078714 Drosophila
28	55.6	10.8	920	8	AZ691914 ENTM026TR
29	55.4	10.8	733	8	AZ820077 2M0092M04
30	55.4	10.8	781	9	AG565560 Mus muscu
31	55.2	10.7	761	9	AG405712 Mus muscu
32	55.2	10.7	1187	9	AG387118 Mus muscu
33	55.2	10.7	1497	9	AG280488 Mus muscu
34	55	10.7	298	9	CE521047 tigr-g88-BH062219 RPCI-24-3
35	55	10.7	519	8	CE451752 tigr-g88-AZ912416 RPCI-24-1
36	55	10.7	606	9	CE451752 tigr-g88-AZ600028 1M0416J09
37	55	10.7	625	8	AZ600028 1M0416J09
38	55	10.7	667	8	AZ600028 1M0416J09
39	55	10.7	675	9	CE006669 tigr-g88-AV728560 AV728560
40	55	10.7	698	1	AV728560 Rattus no
41	55	10.7	3276	3	AY325247 Rattus no
42	54.8	10.6	691	8	BH040136 RPCI-24-2
43	54.8	10.6	776	8	BH044827 RPCI-24-2
44	54.6	10.6	551	9	CE136192 tigr-g88-CE524492
45	54.6	10.6	614	9	CE524492 tigr-g88-

ALIGNMENTS

RESULT 1
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LOCUS
DEFINITION RPCI-23-234D14.TV RPCI-23 Mus musculus genomic clone
ACCESSION RPCI-23-234D14, genomic survey sequence.
VERSION AZ702081.1 GI:12425141
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE Zhao,S., Nierman,W., Feldblum,T., Malek,J., Shatsman,S.,
1 (bases 1 to 537)
AUTHORS Aktner,B., Levine,M., McGann,S., Tsegaye,G., Geer,K., Krol,M., de
Jong,P. and Fraser,C.M.
TITLE Mouse BAC End Sequences from Library RPCI-23
JOURNAL Unpublished (1999)
COMMENT Other GSSs: RPCI-23-234D14.TJ
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
7712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
Fax: 301 838 0208
Email: szhao@tigr.org
Bases are derived from the mouse BAC library RPCI-23. For BAC
library availability, please contact Pieter de Jong
(pdejong@mail.choi.org). Clones may be purchased from BACPAC
Resources (<http://www.choi.org/bacpac/ordering.htm>). BAC end
page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
Plate: 234 row: D column: 14
Seq primer: T7
Class: BAC ends.
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/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="RPCI-23-234D14"
/sex="female"
/lab_host="DH10B"
/clone_lib="RPCI-23"
/note="Organ: Kidney/Brain; Vector: pBACet.6; Site 1:
BACR; Site 2: EcoRI; Female C57BL/6J mouse kidney and/or
brain genomic DNA was isolated and partially digested

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OM nucleic - nucleic search, using SW model

Run on: January 5, 2005, 00:56:14 ; Search time 437 Seconds

(without alignments)
6656.411 Million cell updates/sec

Title: US-09-963-803-2

Perfect score: 515
Sequence: 1 ccagaaggaattatccaag.....cagaagaatttgaatttc 515

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4176236 seqs, 2824127955 residues

Total number of hits satisfying chosen parameters: 8352472

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications NA:*

- 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
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- 5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
- 10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
- 12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
- 13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
- 14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
- 15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
- 16: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
- 17: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
- 18: /cgn2_6/ptodata/1/pubpna/US10F_NEW_PUB.seq:*
- 19: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
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- 21: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	515	100.0	8357	16	US-10-415-302-72
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7	515	100.0	12201	16	US-10-415-302-74
8	515	100.0	12201	16	US-10-415-302-75
9	515	100.0	12201	16	US-10-415-302-76
10	515	100.0	12201	16	US-10-415-302-77
11	515	100.0	12201	16	US-10-415-302-78
12	515	100.0	12201	16	US-10-415-302-79
13	515	100.0	12201	16	US-10-415-302-80
14	515	100.0	12201	16	US-10-415-302-81
15	515	100.0	12201	16	US-10-415-302-82
16	515	100.0	12201	16	US-10-415-302-83
17	515	100.0	12201	16	US-10-415-302-84
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19	515	100.0	12201	16	US-10-415-302-86
20	515	100.0	12201	16	US-10-415-302-87
21	515	100.0	12201	16	US-10-415-302-88

13	120.6	23.4	392	10	US-09-963-803-21
14	120.6	23.4	393	10	US-09-963-803-19
15	120.6	23.4	462	10	US-09-963-803-20
16	120.6	23.4	600	10	US-09-963-803-22
17	120.6	23.4	9285	10	US-09-845-064-52
18	120.6	23.4	15077	10	US-09-845-064-57
19	113	21.9	604	10	US-09-963-803-23
20	110.8	21.5	301	10	US-09-963-803-7
21	110.8	21.5	348	10	US-09-963-803-4
22	110.8	21.5	398	10	US-09-963-803-6
23	108.4	21.0	472	10	US-09-963-803-25
24	108.4	21.0	541	10	US-09-963-803-24
25	62	12.0	62	10	US-09-963-803-10
26	57	11.1	224112	17	US-10-367-094-80
27	56.8	11.0	289190	17	US-10-322-281-115
28	56.2	10.9	948	14	US-10-012-6008-105
29	55	10.7	472	18	US-10-674-1244-5858
30	54	10.5	256525	13	US-10-087-192-451
31	52.6	10.2	298	9	US-09-864-761-18143
32	51.8	10.1	131673	18	US-10-723-860-4422
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36	51.2	9.9	563	18	US-10-357-930-50743
37	51.2	9.9	803	17	US-10-437-963-72176
38	51	9.9	8895	9	US-09-764-853-887
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40	51	9.9	8895	14	US-10-091-438-250
41	51	9.9	8895	14	US-10-091-438-256
42	51	9.9	9656	9	US-09-764-853-886
43	51	9.9	9656	9	US-09-764-853-933
44	51	9.9	9656	14	US-10-091-438-246
45	51	9.9	9656	14	US-10-091-438-255

ALIGNMENTS

RESULT 1
US-09-963-803-2
; Sequence 2, Application US/09963803
; Publication No. US20030028922A1
; GENERAL INFORMATION:
; APPLICANT: Meristem Therapeutics
; TITLE OF INVENTION: Chimeric expression promoters originating from commelina yell
; FILE REFERENCE: 184332042
; CURRENT APPLICATION NUMBER: US/09/963, 803
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: FR 99/03925
; PRIOR FILING DATE: 1999-03-29
; PRIOR APPLICATION NUMBER: PCT IB00/00370
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 515
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURES:
; OTHER INFORMATION: of 515 bp in length EMBL
; NAME/KEY: Promoter
; LOCATION: (1) (515)
; OTHER INFORMATION:
US-09-963-803-2

vi:

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OM nucleic - nucleic search, using sw model

Run on: January 5, 2005, 01:00:34 ; Search time 87 Seconds
(without alignments)
4207.543 Million cell updates/sec

Title: US-09-963-803-2

Perfect score: 515
Sequence: 1 ccagaaggaattatccaaag.....cagaagaattcgaatttg 515

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 4: /cgn2_6/ptodata/1/ina/6B.COMB.seq:*
- 5: /cgn2_6/ptodata/1/ina/6C.COMB.seq:*
- 6: /cgn2_6/ptodata/1/ina/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	513.4	99.7	853	US-09-641-466-2	Sequence 2, Appli
3	511.8	99.4	12241	US-09-948-128-4	Sequence 4, Appli
4	511.4	99.3	8340	US-09-847-057-4	Sequence 4, Appli
5	511.4	99.3	8340	US-09-874-926-4	Sequence 4, Appli
6	427	82.9	593	US-09-641-466-3	Sequence 3, Appli
7	427	82.9	857	US-09-641-466-4	Sequence 4, Appli
8	427	82.9	931	US-09-641-466-5	Sequence 5, Appli
9	332	64.5	931	US-09-641-466-6	Sequence 6, Appli
10	332	64.5	931	US-09-641-466-6	Sequence 6, Appli
11	76	14.8	7218	US-08-232-463-14	Sequence 14, Appli
12	44.6	8.7	3279	US-08-446-137B-1	Sequence 1, Appli
13	43.8	8.5	152331	US-09-128-155-16	Sequence 16, Appli
14	43.2	8.4	929	US-09-671-317-14	Sequence 14, Appli
15	43.2	8.4	1001	US-09-671-317-439	Sequence 439, App
16	42.8	8.3	106746	US-09-326-402C-1	Sequence 1, Appli
17	42.8	8.3	106746	US-09-326-402C-12	Sequence 12, Appli
18	42.6	8.3	5433	US-09-929-329-1	Sequence 1, Appli
19	42.4	8.2	5455	US-10-204-708-34	Sequence 34, Appli
20	42.2	8.2	478	US-09-621-976-10407	Sequence 10407, A
21	42.2	8.2	696	US-09-461-697-193	Sequence 193, App
22	42.2	8.2	699	US-09-461-697-191	Sequence 191, App
23	42.2	8.2	717	US-09-461-697-189	Sequence 189, App
24	42.2	8.2	774	US-09-461-697-185	Sequence 185, App
25	42.2	8.2	819	US-09-461-697-184	Sequence 184, App
26	42.2	8.2	1659	US-09-128-155-17	Sequence 17, Appli
27	42.2	8.2	176373	US-09-128-155-17	Sequence 17, Appli

28	41.4	8.0	1359	US-09-248-796A-1541	Sequence 1541, Ap
29	41.2	8.0	188	US-08-115-497-21	Sequence 21, Appli
30	41.2	8.0	188	US-08-466-670-21	Sequence 21, Appli
31	41.2	8.0	188	US-08-291-011-1	Sequence 1, Appli
32	41.2	8.0	188	US-09-266-065-1	Sequence 1, Appli
33	41.2	8.0	188	US-09-935-247-1	Sequence 1, Appli
34	41.2	8.0	405	US-08-239-074A-1	Sequence 1, Appli
35	41.2	8.0	405	US-09-359-773-1	Sequence 1, Appli
36	41.2	8.0	843	US-09-248-796A-5393	Sequence 5393, Ap
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40	41.2	8.0	2223	US-08-257-073-4	Sequence 4, Appli
41	41.2	8.0	3211	US-08-574-959A-8	Sequence 8, Appli
42	41.2	8.0	3211	US-09-357-014-8	Sequence 8, Appli
43	41.2	8.0	3574	US-09-446-504-83	Sequence 83, Appli
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45	41.2	8.0	3901	US-08-574-959A-6	Sequence 6, Appli

ALIGNMENTS

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RESULT 1
US-09-641-466-1
/ Sequence 1, Application US/09641466
/ Patent No. 6664384
/ GENERAL INFORMATION:
/ APPLICANT: Xu, Dongmei
/ TITLE OF INVENTION: Duplicated Cassava Vein Mosaic Virus
/ FILE REFERENCE: 07678/078002
/ CURRENT APPLICATION NUMBER: US/09/641,466
/ NUMBER OF SEQ ID NOS: 6
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 1
/ LENGTH: 515
/ TYPE: DNA
/ ORGANISM: cassava vein mosaic virus
US-09-641-466-1

Query Match      99.7%; Score 513.4; DB 4; Length 515;
Best Local Similarity 99.8%; Pred. No. 4.6e-124;
Matches 514; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCGAAGGTAAATTCACAGATGATGATCAATTCATGTTTACGGGAAAACATATG 60
DB 1 CCGAAGGTAAATTCACAGATGATGATCAATTCATGTTTACGGGAAAACATATG 60

QY 61 GAAGTATTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 120
DB 61 GAAGTATTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 120

QY 121 TCAAAATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 180
DB 121 TCAAAATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 180

QY 181 GTGAATTTGAAAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 240
DB 181 GTGAATTTGAAAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 240

QY 241 GACAAAGTAAAGAAAGAAAGAAAGAAAGTAAAGTAAAGTAAAGTAAAGTAAAG 300
DB 241 GACAAAGTAAAGAAAGAAAGAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAG 300

QY 301 GTAAAGTGAAGAAATGTAAGGCGGAAAGTAACTTATCAAAAGAAATCTTATCC 360
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QY 361 TACTTATCTTTTATATTTTCCGTCAATTTTGCCTTGAAGTTTCTATTAAGAA 420
DB 361 TACTTATCTTTTATATTTTCCGTCAATTTTGCCTTGAAGTTTCTATTAAGAA 420
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 5, 2005, 00:38:49 ; Search time 413 Seconds
(without alignments)
6545.888 Million cell updates/sec

Title: US-09-963-803-2
Perfect score: 515
Sequence: 1 ccagaagtgtaattacgaag.....cagagaacttgcgaatttg 515

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 413486 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 1: geneseqn1980s:*
- 2: geneseqn1990s:*
- 3: geneseqn2000s:*
- 4: geneseqn2001as:*
- 5: geneseqn2001bs:*
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- 8: geneseqn2003as:*
- 9: geneseqn2003bs:*
- 10: geneseqn2003cs:*
- 11: geneseqn2003ds:*
- 12: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	515	100.0	515	3	AAA96836
2	515	100.0	532	4	AAD11575
3	515	100.0	538	12	AD085792
4	515	100.0	538	12	AD059549
5	515	100.0	538	12	AD054812
6	515	100.0	1839	6	ABL57988
7	515	100.0	4677	6	ABL57989
8	515	100.0	8187	6	ABL58082
9	514	99.8	1052	6	AB553107
10	514	99.8	1590	6	AB553109
11	513.4	99.7	515	4	AAF55505
12	513.4	99.7	524	2	AAV14020
13	513.4	99.7	526	2	AAV14018
14	513.4	99.7	853	4	AAF55506
15	511.8	99.4	12241	6	AA073049
16	511.8	99.4	12241	6	AA073049
17	511.8	99.4	12241	11	AD005418
18	511.4	99.3	8340	6	AA024139
19	511.4	99.3	8340	6	AA024139
20	461	89.5	1590	6	AB553109
21	431.8	83.8	491	2	AAV14030

22	427	82.9	593	4	AAF55507	AAF55507 Nucleotid
23	427	82.9	857	4	AAF55508	AAF55508 Nucleotid
24	427	82.9	931	4	AAF55509	AAF55509 Nucleotid
25	412.2	80.0	482	2	AAV14027	AAV14027 CbVNV pro
26	401.8	78.0	476	2	AAV14053	AAV14053 CbVNV pro
27	401.2	77.9	411	2	AAV14021	AAV14021 CbVNV pro
28	392	76.1	392	2	AAV14019	AAV14019 CbVNV pro
29	390.2	75.8	710	12	AD059550	AD059550 Double Cs
30	390.2	75.8	710	12	AD054813	AD054813 Cassava v
31	385.8	74.9	468	2	AAV14029	AAV14029 CbVNV pro
32	365.8	71.0	458	2	AAV14028	AAV14028 CbVNV pro
33	333.4	64.7	441	2	AAV14033	AAV14033 CbVNV pro
34	332	64.5	931	4	AAF55510	AAF55510 Nucleotid
35	332	64.5	931	4	AAF55510	AAF55510 Nucleotid
36	300.4	58.3	420	2	AAV14026	AAV14026 CbVNV pro
37	295.2	57.3	305	2	AAV14022	AAV14022 CbVNV pro
38	285.8	55.5	418	2	AAV14032	AAV14032 CbVNV pro
39	265.8	51.6	408	2	AAV14031	AAV14031 CbVNV pro
40	250.2	48.6	261	2	AAV14023	AAV14023 CbVNV pro
41	219	42.5	219	12	AD059546	AD059546 Cassava v
42	219	42.5	219	12	AD054809	AD054809 Cassava v
43	194	37.7	1052	6	AB553107	AB553107 Transgene
44	194	37.7	1618	6	AB553117	AB553117 Transgene
45	194	37.7	1618	6	AB553117	AB553117 Transgene

ALIGNMENTS

RESULT 1
ID AAA96836 strand; DNA; 515 BP.
XX
AC AAA96836;
DT 19-FEB-2001 (first entry)
XX
DE Promoter from intergenic region of Cassava vein mosaic virus.
XX
KW Promoter; intergenic region; Commelina yellow mottle virus;
KW chimeric expression promoter; plant vascular expression promoter;
KW plant green tissue expression promoter; Cassava vein mosaic virus;
KW transgenic plant; ss.
XX
OS Cassava vein mosaic virus.
XX
PN WO200058485-A1.
XX
PD 05-OCT-2000.
XX
PF 29-MAR-2000; 2000MO-IB000370.
XX
PR 29-MAR-1999; 99FR-00003925.
XX
PA (MERI-) MERISTEM THERAPEUTICS.
XX
PI Rance I, Gruber V, Theisen M;
XX
DR WPI; 2000-647238/62.
XX
PT Chimeric expression promoter for transgenic plant production, comprises
PT sequence from promoter comprising vascular expression region replaced
PT with sequence from promoter comprising green tissue expression region.
XX
PS Claim 4; Page 80; 91pp: English.
XX
CC The present sequence represents a promoter fragment from the intergenic
CC region of Cassava vein mosaic virus. The promoter is used to construct
CC chimeric expression promoters. These chimeric promoters comprise a
CC nucleic acid sequence which is derived from a first plant promoter, in
CC which a plant vascular expression promoter region is replaced with a
CC nucleic acid sequence derived from a second plant promoter comprising a
CC plant green tissue expression promoter region. Preferably, the first

